

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/586,978
Source: IFWP
Date Processed by STIC: 08/03/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 08/03/2006

PATENT APPLICATION: US/10/586,978

TIME: 09:46:39

Input Set : F:\SEQLIST.TXT

Output Set: N:\CRF4\08032006\J586978.raw

3 <110> APPLICANT: Kohonen-Corish, Maija
 5 <120> TITLE OF INVENTION: Methods of diagnosing colorectal cancer and reagents therefor

7 <130> FILE REFERENCE: RICE-029
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/586,978
 C--> 9 <141> CURRENT FILING DATE: 2006-07-20
 9 <150> PRIOR APPLICATION NUMBER: AU 2004900340
 10 <151> PRIOR FILING DATE: 2004-01-23
 12 <150> PRIOR APPLICATION NUMBER: US 60/540,662
 13 <151> PRIOR FILING DATE: 2004-01-29
 15 <150> PRIOR APPLICATION NUMBER: PCT/AU2005/000077
 16 <151> PRIOR FILING DATE: 2005-01-24
 18 <160> NUMBER OF SEQ ID NOS: 46
 20 <170> SOFTWARE: PatentIn version 3.3
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 4181
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (221)..(2707)
 32 <400> SEQUENCE: 1

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37	tgtggcagaa gggaccaagc agtggatatt gagcctgtga agtccaactc ttaagctccg	180
39	agacctgggg gactgagagc ccagctctga aaagtgcacg atg aat tcc gga gtt	235
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43	gcc atg aaa tat gga aac gac tcc tcg gcc gag ctg agt gag ctc cat	283
44	Ala Met Lys Tyr Gly Asn Asp Ser Ser Ala Glu Leu Ser Glu Leu His	
45	10 15 20	
47	tca gca gcc ctg gca tca cta aag gga gat ata gtg gaa ctt aat aaa	331
48	Ser Ala Ala Leu Ala Ser Leu Lys Gly Asp Ile Val Glu Leu Asn Lys	
49	25 30 35	
51	cgt ctc cag caa aca gag agg gaa cgg gac ctt ctg gaa aag aaa ttg	379
52	Arg Leu Gln Gln Thr Glu Arg Glu Arg Asp Leu Leu Glu Lys Lys Leu	
53	40 45 50	
55	gcc aag gca cag tgc gag cag tcc cac ctc atg aga gag cat gag gat	427
56	Ala Lys Ala Gln Cys Glu Gln Ser His Leu Met Arg Glu His Glu Asp	
57	55 60 65	
59	gtc cag gag cga acg acg ctt cgc tat gag gaa cgc atc aca gag ctc	475
60	Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu Arg Ile Thr Glu Leu	
61	70 75 80 85	
63	cac agc gtc att gcg gag ctc aac aag aag ata gac cgt ctg caa ggc	523

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67 acc acc atc agg gag gaa gat gag tac tca gaa ctg cga tca gaa ctc      571
68 Thr Thr Ile Arg Glu Glu Asp Glu Tyr Ser Glu Leu Arg Ser Glu Leu
69          105          110          115
71 agc cag agc caa cac gag gtc aac gag gac tct cga agc atg gac caa      619
72 Ser Gln Ser Gln His Glu Val Asn Glu Asp Ser Arg Ser Met Asp Gln
73          120          125          130
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76 Asp Gln Thr Ser Val Ser Ile Pro Glu Asn Gln Ser Thr Met Val Thr
77          135          140          145
79 gct gac atg gac aac tgc agt gac ctg aac tca gaa ctg cag agg gtg      715
80 Ala Asp Met Asp Asn Cys Ser Asp Leu Asn Ser Glu Leu Gln Arg Val
81 150          155          160          165
83 ctg aca ggg ctg gag aat gtt gtc tgc ggc agg aag aag agc agc tgc      763
84 Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg Lys Lys Ser Ser Cys
85          170          175          180
87 agc ctc tcc gtg gcc gag gtg gac agg cac att gag cag ctc acc aca      811
88 Ser Leu Ser Val Ala Glu Val Asp Arg His Ile Glu Gln Leu Thr Thr
89          185          190          195
91 gcc agc gag cac tgt gac ctg gct att aag aca gtc gag gag att gag      859
92 Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr Val Glu Glu Ile Glu
93          200          205          210
95 ggg gtg ctt ggc cgg gac ctg tat ccc aac ctg gct gaa gag agg tct      907
96 Gly Val Leu Gly Arg Asp Leu Tyr Pro Asn Leu Ala Glu Glu Arg Ser
97          215          220          225
99 cgg tgg gag aag gag ctg gct ggg ctg agg gaa gag aat gag agc ctg      955
100 Arg Trp Glu Lys Glu Leu Ala Gly Leu Arg Glu Glu Asn Glu Ser Leu
101 230          235          240          245
103 act gcc atg ctg tgc agc aaa gag gaa gaa ctg aac cgg act aag gcc      1003
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107 acc atg aat gcc atc cgg gaa gag cgg gac cgg ctc cgg agg cgg gtc      1051
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111 aga gag ctt caa act cga cta cag agc gtg cag gcc aca ggt ccc tcc      1099
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115 agc cct ggc cgc ctc act tcc acc aac cgc ccg att aac ccc agc act      1147
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117          295          300          305
119 ggg gag ctg agc aca agc agc agc agc aat gac att ccc atc gcc aag      1195
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123 att gct gag agg gtg aag cta tca aag aca agg tcc gaa tcg tca tca      1243
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128 Ser Asp Arg Pro Val Leu Gly Ser Glu Ile Ser Ser Ile Gly Val Ser

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135	atc caa gag att ttc caa aca ctc tac tca cac gga tct gcc atc tca	1387		
136	Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His Gly Ser Ala Ile Ser			
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139	gaa agc aag att aga gag ttt gag gtg gaa aca gaa cgg ctg aat agc	1435		
140	Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr Glu Arg Leu Asn Ser			
141	390 395 400 405			
143	cgg att gag cac ctc aaa tcc caa aat gac ctc ctg acc ata acc ttg	1483		
144	Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu Leu Thr Ile Thr Leu			
145	410 415 420			
147	gag gaa tgt aaa agc aat gct gag agg atg agc atg ctg gtg gga aaa	1531		
148	Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser Met Leu Val Gly Lys			
149	425 430 435			
151	tac gaa tcc aat gcc aca gcg ctg agg ctg gcc ttg cag tac agc gag	1579		
152	Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala Leu Gln Tyr Ser Glu			
153	440 445 450			
155	cag tgc atc gaa gcc tac gaa ctc ctc ctg gcg ctg gca gag agt gag	1627		
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157	455 460 465			
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161	470 475 480 485			
163	cct gga gac cag tgc ggg gat gaa aac atc act cag atg ctc aag cga	1723		
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168	Ala His Asp Cys Arg Lys Thr Ala Glu Asn Ala Ala Lys Ala Leu Leu			
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177	535 540 545			
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188	Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser Ile His Ile Asp Pro			
189	585 590 595			
191	ctc agc tat gac gtc aag cct cgg gga gac agc cag agg ctg gat ctg	2059		
192	Leu Ser Tyr Asp Val Lys Pro Arg Gly Asp Ser Gln Arg Leu Asp Leu			
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203	ctg gag ctg aag ctg agc acg cgg gag gcc cag gag cag gcc tac ctg	2203
204	Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln Glu Gln Ala Tyr Leu	
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208	Val His Ile Glu His Leu Lys Ser Glu Val Glu Glu Gln Lys Glu Gln	
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211	cgg atg cga tcc ctc agc tcc acc agc agc ggc agc aaa gat aaa cct	2299
212	Arg Met Arg Ser Leu Ser Ser Thr Ser Ser Gly Ser Lys Asp Lys Pro	
213	680 685 690	
215	ggc aag gag tgt gct gat gct gcc tcc cca gct ctg tcc cta gct gaa	2347
216	Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala Leu Ser Leu Ala Glu	
217	695 700 705	
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221	710 715 720 725	
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237	775 780 785	
239	tta gag tcg cag atg atg gcc atg gtg gag aga cat gag acc caa gtg	2635
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241	790 795 800 805	
243	agg atg ctc aag caa aga ata gct ctg cta gag gag gag aac tcc agg	2683
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Output Set: N:\CRF4\08032006\J586978.raw

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302 <210> SEQ ID NO: 2

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304 <212> TYPE: PRT

305 <213> ORGANISM: Homo sapiens

307 <400> SEQUENCE: 2

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318 35 40 45
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322 50 55 60
325 Arg Glu His Glu Asp Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu
326 65 70 75 80
329 Arg Ile Thr Glu Leu His Ser Val Ile Ala Glu Leu Asn Lys Lys Ile
330 85 90 95
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334 100 105 110
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338 115 120 125
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342 130 135 140
345 Ser Thr Met Val Thr Ala Asp Met Asp Asn Cys Ser Asp Leu Asn Ser
346 145 150 155 160
349 Glu Leu Gln Arg Val Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg
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357 Glu Gln Leu Thr Thr Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/586,978

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Input Set : F:\SEQLIST.TXT
Output Set: N:\CRF4\08032006\J586978.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 9521

VERIFICATION SUMMARY

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Input Set : F:\SEQLIST.TXT

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:9467